

FIG. 1A

1	CCCACGCGTCCGATTAAAGTGAGGAGAGAGCTACAAACCAAGTAAGCAAGTGTCAAGGGCTC	60
61	ACCAACCATGCAAGGCAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTGTTCCAA	120
1	<u>M Q G Q G R R R G T C K D I F C S K</u>	18
121	AATGGCATCTTACCTTATGGAGTACTCTTGCTGTTGGCCTCTGTGCTCCAATCTACTG	180
19	<u>M A S Y L Y G V L F A V G L C A P I Y C</u>	38
181	TGTGTCCCCGGCCAATGCCCGACTGCAACACCGACTTTGCCTCCGCCTACCGCAGGGCTGGT	240
39	<u>V S P A N A P S A Y P R P S S T K S T P</u>	58
241	TGCCTCACAGGTGTATTCCCTCAACACCGACTTTGCCTCCGCCTACCGCAGGGCTGGT	300
59	<u>A S Q V Y S L N T D F A F R L Y R R L V</u>	78
301	TTTGGAGACCCCGAGTCAGAACATCTCTTCTCCCGTGTGAGTGTCTCCACCTCCCTGGC	360
79	<u>L E T P S Q N I F F S P V S V S T S L A</u>	98
361	CATGCTCTCCCTGGGCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGCTT	420
99	<u>M L S L G A H S V T K T Q I L Q G L G F</u>	118
421	CAACCTCACACACACACCAGAGTCTGCCATCCACCCAGGGCTTCCAGCACCTGGTTCACTC	480
119	<u>N L T H T P E S A I H Q G F Q H L V H S</u>	138
481	ACTGACTGTTCCAGCAAAGACCTGACCTTGAAGATGGAAAGTGCCCTTCGTCAAGAA	540
139	<u>L T V P S K D L T L K M G S A L F V K K</u>	158
541	GGAGCTGCAGCTGCAGGCAAATTCTGGCAATGTCAAGAGGCTGTATGAAGCAGAAAGT	600
159	<u>E L Q L Q A N F L G N V K R L Y E A E V</u>	178
601	CTTTTCTACAGATTCTCAAACCCCTCATTGCCAGGCGAGGATCAACAGCCATGTGAA	660
179	<u>F S T D F S N P S I A Q A R I N S H V K</u>	198
661	AAAGAAGACCCAAAGGGAGGTTGTAGACATAATCCAAGGCCTTGACCTCTGACGCCAT	720
199	<u>K K T Q G K V V D I I Q G L D L L T A M</u>	218
721	GGTTCTGGTGAATCACATTCTTAAAGCCAAGTGGAGAAGCCCTTCACCTTGAATA	780
219	<u>V L V N H I F F K A K W E K P F H L E Y</u>	238
781	TACAAGAAAGAACTTCCCATTCTGGTGGCGAGCAGGTCACTGTGCAAGTCCCCATGAT	840
239	<u>T R K N F P F L V G E Q V T V Q V P M M</u>	258
841	GCACCAGAAAGAGCAGTCGCTTGGGTGGATACAGAGCTGAACGTGCTTGTGCTGCA	900
259	<u>H Q K E Q F A F G V D T E L N C F V L Q</u>	278

FIG. 1B

901	GATGGATTACAAGGGAGATGCCGTGGCCTTCTTGTCCCTCCCTAGCAAGGGCAAGATGAG	960
279	M D Y K G D A V A F F V L P S K G K M R	298
961	GCAACTGGAACAGGCCTTGTCAGCCAGAACACTGATAAAAGTGGAGCCACTCACTCCAGAA	1020
299	Q L E Q A L S A R T L I K W S H S L Q K	318
1021	AAGGTGGATAGAGGTGTTCATCCCCAGATTTCCATTCTGCCCTACAAATCTGGAAAC	1080
319	R W I E V F I P R F S I S A S Y N L E T	338
1081	CATCCTCCCGAAGATGGGCATCCAAAATGCCCTTGACAAAAATGCTGATTTCTGGAAT	1140
339	I L P K M G I Q N A F D K N A D F S G I	358
1141	TGCAAAGAGAGACTCCCTGCAGGTTCTAAAGCAACCCACAAGGCTGTGCTGGATGTCAG	1200
359	A K R D S L Q V S K A T H K A V L D V S	378
1201	TGAAGAGGGCACTGAGGCCACAGCAGTACCAACCAAGTTCATAGTCCGATCGAAGGA	1260
379	E E G T E A T A A T T T K F I V R S K D	398
1261	TGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCTGATGATGATTACAATAA	1320
399	G P S Y F T V S F N R T F L M M I T N K	418
1321	AGCCACAGACGGTATTCTCTTCTAGGGAAAGTGGAAATCCACTAAATCCTAGGTGGG	1380
419	A T D G I L F L G K V E N P T K S *	436
1381	AAATGGCCTGTTAATGATGGCACATTGCTAATGCACAAGAAATAACAAACCACATCCCT	1440
1441	CTTTCTGTTCTGAGGGTGCATTGACCCAGTGGAGCTGGATTCGCTGGCAGGGATGCCA	1500
1501	CTTCCAAGGCTCAATCACCAAAACCATCAACAGGGACCCCAGTCACAAGCCAACACCCATT	1560
1561	AACCCCAGTCAGTGCCCTTTCCACAAATTCTCCAGGTAACTAGCTTCAATGGATGTTG	1620
1621	CTGGGTTACCATATTCCATTCTGGGCTCCAGGAATGAAATACGCCAACCCAGGT	1680
1681	TAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAAACTAAAATATGAAAAAAA	1740
1741	AAAAAAAAAAAAAAAAAAAAAAA 1766	

FIG. 2

AL132708_FL	1	50
AACT_HUMAN	(1) MQGQGRRRGTCDFCSKMASYLGYV EFAVCECAPIYCVSPANAPSAYPR	
KAIN_HUMAN	(1) -----MERMLPELALCEAGFCPAVLCHPNPLD	
THBG_HUMAN	(1) -----MHLIDYLLLLVEALSHGQLHVEHDGESCS	
	-----MSPFLYLVLLVLGEATIHCASPEGKVTACHS	
AL132708_FL	51	100
AACT_HUMAN	(51) PS-----STKSTPASQVYSLNT DFAFRLYRRLVLET PSQNIFF SPVSV	
KAIN_HUMAN	(31) EENLTQENQDRGTHV DLGLASANVDF AFASLYKQLVLKAPDKNVI ESPLSI	
THBG_HUMAN	(33) NSSHQQILET GEGSPSLKIA APANAD DFRFY YLIASE TPGKNI FF SPLSI	
	(33) -----SQPNATLYKMSSINA DF DFNLYR RT VETPDKNI FF SPVSI	
AL132708_FL	101	150
AACT_HUMAN	(94) STSLAM LSLG AHSVTKTQ ILQGLGF NE HTPESAIHQG FO HLVH SETVPS	
KAIN_HUMAN	(81) STALAF LSLG AHNT TLTE ILKGLK ENI ET SEAEIHQS FO HLR T ENQSS	
THBG_HUMAN	(83) SAAYAM LSLG ACSHRSQ TLEG LF GENI TE LES SDVHRG FO HLH T ENLPG	
	(74) SAALV M LSFG ACC ST QTE IV ETL GEN ITD TP MEI Q HG FO HLIC SEN FPK	
AL132708_FL	151	200
AACT_HUMAN	(144) K DTL K MGS AL EVK K ELQ Q AN E LG N V K R L Y E A E V E ST D E S N P S I A Q A R I	
KAIN_HUMAN	(131) D E QL LSM G NAME V KE Q L S LLD R F TE DA K R L Y G SE A F A T D F Q D S AA A K L I	
THBG_HUMAN	(133) H G LE TRV G SA E EL SH N E K FL A K FL LN D TM A V Y AK L E H T N F Y D T V G T I QL I	
	(124) K E E E L Q I G N A L I F G K H L K P L A K E L N D V K T L Y E T E V E ST D E S N I A A K Q E I	
AL132708_FL	201	250
AACT_HUMAN	(194) N SHV KK K TO G K V V D II IQG ED LL T AM V I V NH I F E K A K W E K P F HE Y TR K N F	
KAIN_HUMAN	(181) N DY V KNG T R G K I T D L I D S Q T MM V I V NY I F E K A K W E M P D P Q D TH Q S R	
THBG_HUMAN	(183) N DH V KK E TR G K I V D L V SE I KK D V L M V I V NY I F E K A K W E K P FI S RT P K D	
	(174) N SHV E MQ T K G V V G L I Q D E K P N T I M V I NY I H F K A Q W A N P F D P S K T E D S S	
AL132708_FL	251	300
AACT_HUMAN	(244) P F L V GE Q V T V Q V P MM H Q K E Q F A G V D T E I N C F V L Q M D Y K G D A V F V I P S	
KAIN_HUMAN	(231) F Y LS KK K W V M V P MM L Q D Q E HH W Y L H E R Y L P C S V L R M D Y K G D A T V F E I P N	
THBG_HUMAN	(233) F Y V D E N T T V R V P MM L Q D Q E HH W Y L H E R Y L P C S V L R M D Y K G D A T V F E I P N	
	(224) S F L I D K T TT T V Q V P MM H Q M E Q Y Y H L V D M E I N C T V L Q M D Y S K N A L A E V E P K	
AL132708_FL	301	350
AACT_HUMAN	(294) K G K M R Q L E Q A S A T L I K W H S L Q K R --- W I E V F I P R E S I S A S Y N L E T I	
KAIN_HUMAN	(281) Q D K M E E V A M L L P E T L K R W R D S L E F R --- E I G E L Y L P K E S I S R D Y N L D I	
THBG_HUMAN	(283) Q G K M R I E E V L T P E M L M R W N N L R K R N F Y K K L E L H L P K E S I S G S Y V L D Q I	
	(274) E G Q M E S V E A A M S S K T I KK W N R L E Q K G --- W V D L F V P K E S I S A T Y D G A T	
AL132708_FL	351	400
AACT_HUMAN	(340) E P K M G I Q N A F D K N A D F G S I A K R D S L Q V S K A T H K A V L D V S E E G T E A A T A A T T	
KAIN_HUMAN	(328) E L Q L G I E E A F T S K A D L S G I T G A R N L A V S Q V V H K A V L D V F E E G T E A S A A T A	
THBG_HUMAN	(333) E P R L G F T D L F S K W A D L S G I T K Q Q K L E A S K F H K A T L D V D E A G T E A A A T T	
	(320) E L K M G I Q H A Y S E N A D F S G L T E D N GL K L S N A A H K A V L H I G E K G T E A A V P E	
AL132708_FL	401	446
AACT_HUMAN	(390) T K F I V R S K D G P S Y F T V S F N R T E L M M I T N K A T D G I L F L G K V E N P T K S	
KAIN_HUMAN	(378) V K I T L S A L V E T R T I V R F N R P E L M I T V P T D T Q N I F M S X V T N P K Q A	
THBG_HUMAN	(383) F A I K F F S A Q T N - R H I L R F N R P E L V V I F S T S T Q S V L E F L G K V V D P T K P	
	(370) V E L S D Q P E N T F L H P I I Q I D R S F M L L I E R S T R S I L F L G K V V N P T E A	

FIG. 3

LSI-01 pdb1qlp	MQGQGRRRG T CKDIFCSKMA SYLYGVLF A V GLCAPIYCVS P A N I P S A Y P R MDPQ GDAQKTDTS
LSI-01 pdb1qlp	PSSTKSTPAS QVYSINTDPA F R R R R E V L E T P S Q N E R F S P V S V S E S L A M E HHDQDHPTFN K I T P N L A E H A K S I M R O H A Q S N S T M E R F S P V S I A M A F A M L
LSI-01 pdb1qlp	SIGAH S V E K T Q E E Q S E G I E N L T H T P E S A T H Q G E C H I V H E S E T V B S K D E T E K M S I G T K A D T H D E F E G E G E N F N L T E I P E A Q H E G E C E L L R T E N Q B D S Q E Q B T T
LSI-01 pdb1qlp	G S A I F V K K E L Q I Q A N E I G N V K R E V E A E V F S T D E S N P S I A Q A R E N S H U K E K G N G E F L S E G L K E V D K M I E D V K G L V H S E A F T V N E G D T E E N K K Q I N D Y M E N G
LSI-01 pdb1qlp	T Q G K V V D I I Q G I D L L T A M V L V N H I G F F K A K W E K P F H L E Y T R K N F P E L V G E Q T Q G K I V D L V K E I D R D T V F A I V N Y I L P F K G K W E R F E V K D T . E E E D E H V D Q V
LSI-01 pdb1qlp	V T V Q V P M M H Q K E Q F A F G V D T E I N C F V E Q M D Y K G D A V A F F V L P S K G I M R Q S T T V K V P M M K R L G M F N I Q H C K K I S S S W V E L M K Y L G N A T A I F F E P D E G K L Q H I
LSI-01 pdb1qlp	E Q A I S A R T L I K W S H S L Q K R W I E V F I P R F S I S A S Y N I E T I L P K M G I Q N A E D E N E L T H D I I T K F L E N E D R R S A S L H L P K L S I T G T Y D L K S V L G Q L G I T K V F S
LSI-01 pdb1qlp	K N A D F S G I A K R D S I Q V S K A T H K A V E D V S E E G T E A T A T A T T T K F I V R S K D G P N G A D L S G V T E E A P I K L S K A V H K A V L T I D E K G T E A A G A M F L E A P P M S I . . .
LSI-01 pdb1qlp	S . Y F T V S F N R T F L M M I T N K A T D G I E F L G K V E N P T K S P E . . . V K F N K P F V F L M I E Q N T K S P L F M G K V V N P T Q K

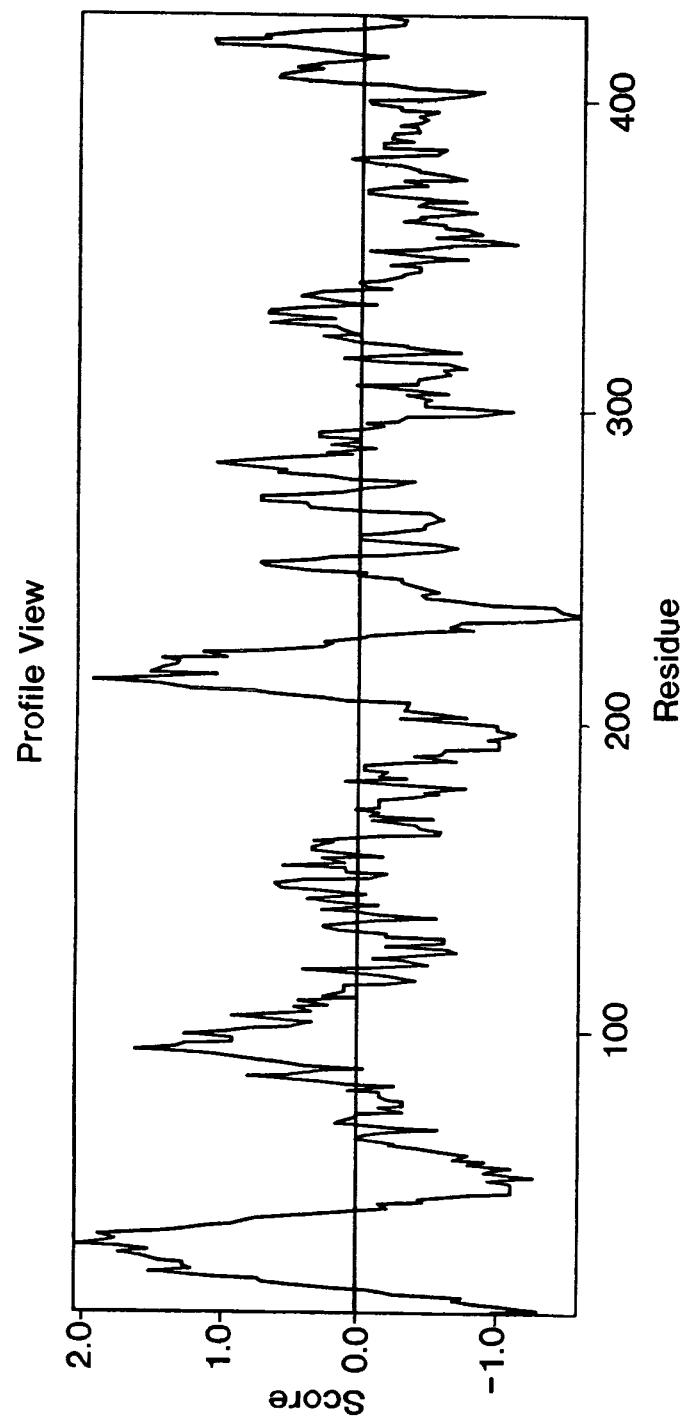


FIG. 4

FIG. 5A

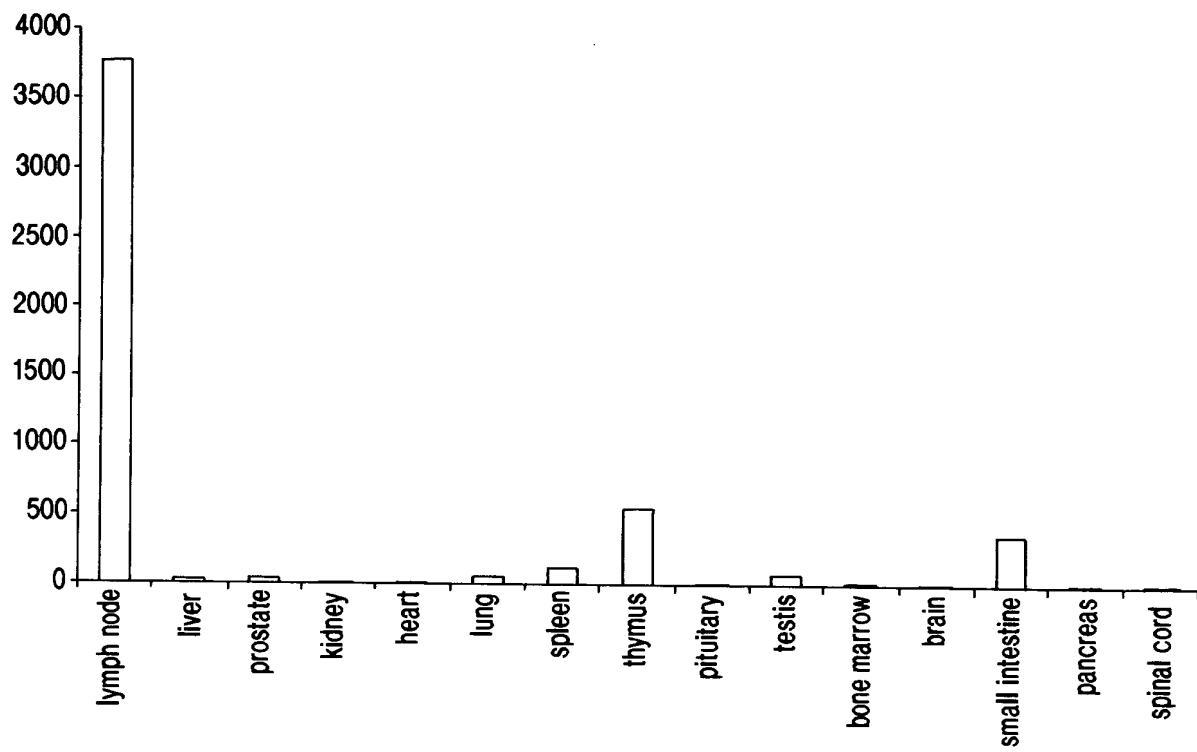


FIG. 5B

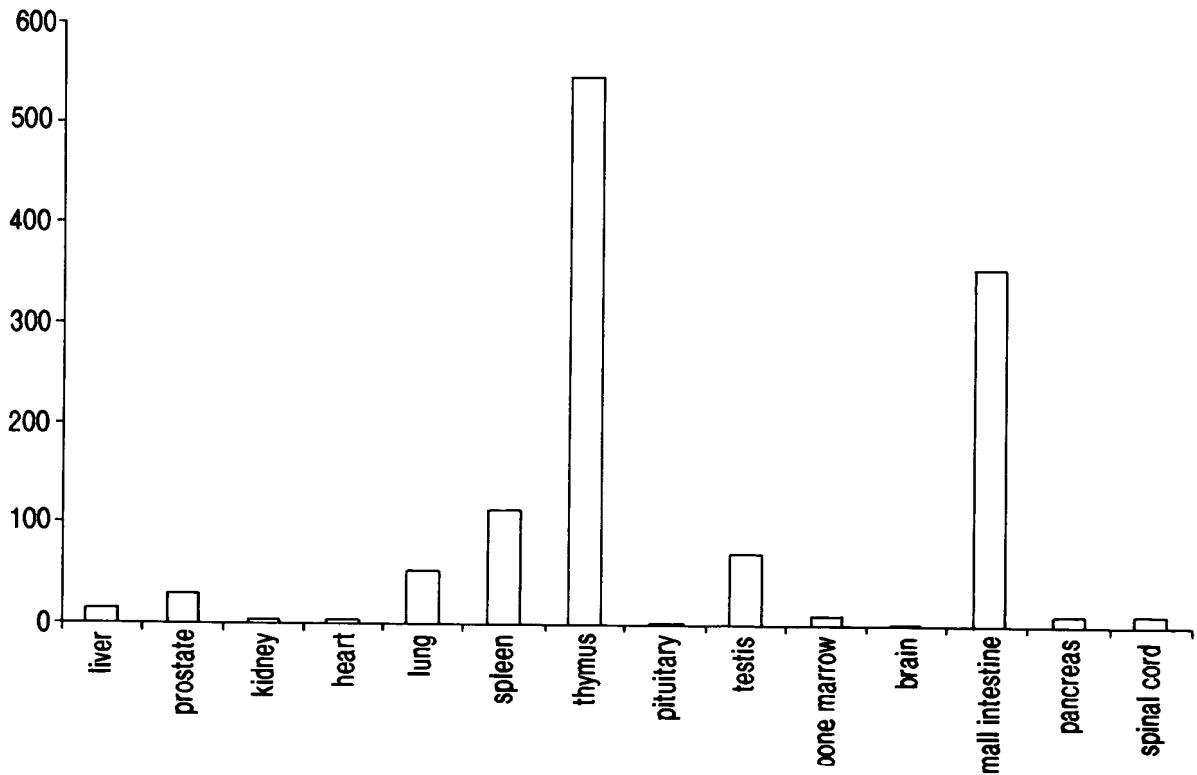


FIG. 6

Protein	Genbank ID	Identities	Similarities
human α_1 -antichymotrypsin	gi 112874	46%	52%
human Kallistatin	gi 5453888	48%	56%
human thyroxin-binding globulin	gi 37142	51%	57%
human α_1 -antitrypsin	gi 6137432	43%	50%

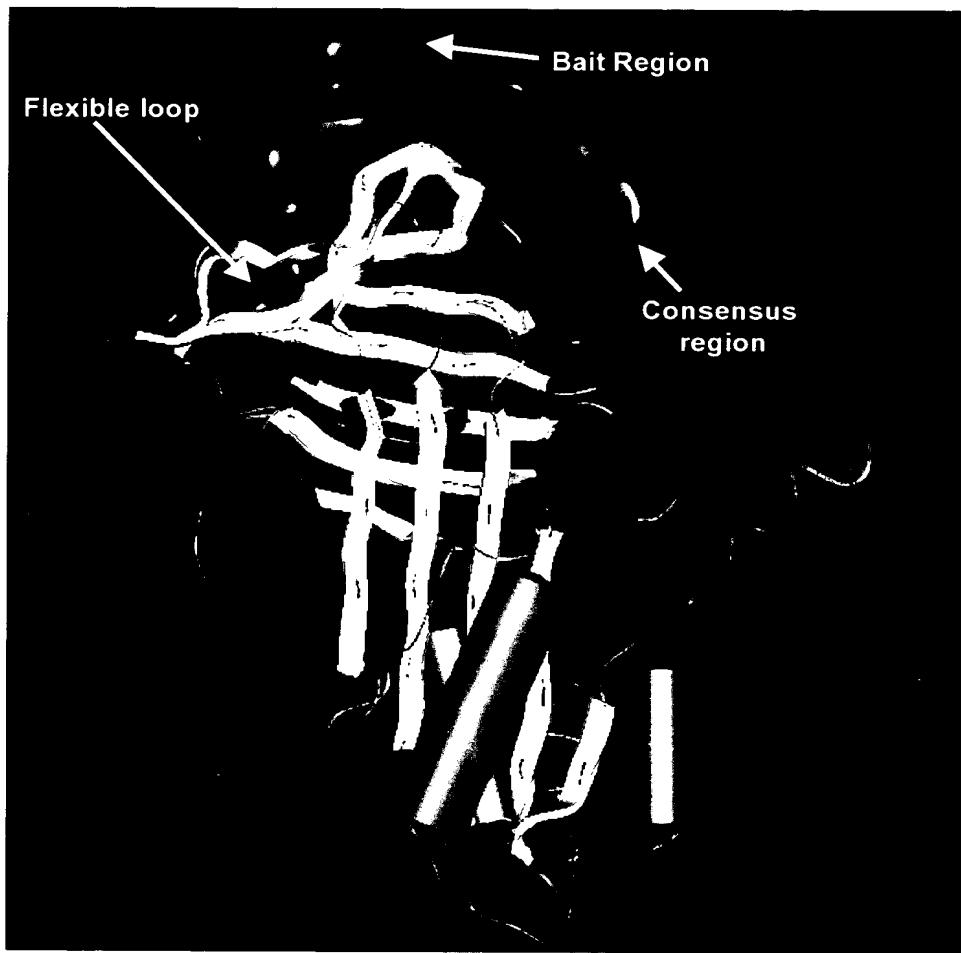


FIG. 7